GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 01:07:03 ; Search time 755.06 Seconds
(without alignments)
29.521 Million cell updates/sec

Title: US-09-851-670-18
Perfect score: 26
Sequence: 1 ttattgtggccatctttgtccagcat 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_1101:*
1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
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4: /SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
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15: /SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn/NA1995.DAT:*
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18: /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	16.2	62.3	31	22	AAI29964	Human single nucle
c	2	15.6	60.0	31	22	AAI29682	Human single nucle
	3	15	57.7	51	22	AAF57498	Oprl gene amplifyi
	4	14.8	56.9	55	14	AAQ49390	PA oligonucleotide
c	5	14.6	56.2	36	20	AAZ10584	PCR primer used to
c	6	14.6	56.2	36	22	AAF77170	Primer F284K. Bac
	7	14.4	55.4	20	21	AAZ44577	Newcastle disease
c	8	14.2	54.6	30	18	AAT50769	Ovine IL-12 40 kD
c	9	14.2	54.6	39	19	AAV13827	Primer for canine
c	10	14.2	54.6	39	20	AAX03165	PCR primer for nuc
c	11	14.2	54.6	39	20	AAX03165	PCR primer used to
	12	14.2	54.6	43	19	AAV16084	PCR primer used to
	13	14.2	54.6	43	21	AAA05400	PCR primer Pax6Mm2
	14	14.2	54.6	43	21	AAZ43415	Murine c-Kit gene
c	15	14.2	54.6	51	22	AAH39264	Human SNP flanking
c	16	14	53.8	27	20	AAZ33239	Alpha-Amy3 promote
c	17	14	53.8	29	15	AAQ56319	5' primer to clone
c	18	14	53.8	40	21	AAZ65203	Probe specific for
c	19	14	53.8	40	22	AAF44360	Human PRO1131 hybr
c	20	14	53.8	40	22	AAC90136	Human PRO polynucl
c	21	14	53.8	41	19	AAV32534	Random oligonucleo
	22	13.8	53.1	19	22	AAS06885	SNP containing pro
c	23	13.8	53.1	46	15	AAQ71345	Antisense primer P
	24	13.8	53.1	51	22	AAH40720	Human SNP flanking
c	25	13.6	52.3	37	21	AAA96800	Nucleotide sequenc
c	26	13.6	52.3	37	21	AAC65024	Cancer detection m
c	27	13.6	52.3	37	22	AAH43906	Human apc gene pro
c	28	13.6	52.3	37	22	AAH43985	Human apc probe ap
c	29	13.6	52.3	37	22	AAF62223	Human adenomatous
c	30	13.6	52.3	47	21	AAZ67851	Human map-related
c	31	13.6	52.3	53	21	AAA62775	Endoglucanase PCR
c	32	13.6	52.3	59	18	AAV79271	Staphylococcus aur
c	33	13.4	51.5	21	22	AAF16563	Gastric acid produ
	34	13.4	51.5	31	19	AAV67700	Nucleotide fragmen
c	35	13.4	51.5	33	22	AAD12827	Human TGF alpha-li
	36	13.4	51.5	39	21	AAA90899	Human tumour necro
	37	13.4	51.5	58	21	AAZ35318	Hepatitis B virus
	38	13.2	50.8	19	18	AAT66258	Primer 2 for hop g
c	39	13.2	50.8	29	20	AAZ32385	Receptor construct
c	40	13.2	50.8	31	19	AAV26189	bIL-12 p40 gene PC
c	41	13.2	50.8	31	22	AAF60070	Primer FLAG-1. Sy
c	42	13.2	50.8	36	19	AAV32525	Trichoderma reesei
	43	13.2	50.8	39	17	AAT43675	Primer-3 used for
	44	13.2	50.8	41	21	AAZ40137	Target sequence LP
	45	13.2	50.8	41	21	AAZ40279	Target probe LP280

ALIGNMENTS

RESULT 1
AAI29964
ID AAI29964 standard; DNA; 31 BP.
XX
AC AAI29964;
XX
DT 18-OCT-2001 (first entry)
XX
DE Human single nucleotide polymorphism (SNP) 49.
XX
KW Human; resequence; genotype; disease; forensic; paternity testing;
KW single nucleotide polymorphism; SNP; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(16,T)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO200166800-A2.
XX
PD 13-SEP-2001.
XX
PF 07-MAR-2001; 2001WO-US07268.
XX
PR 07-MAR-2000; 2000US-0187510.
PR 22-MAY-2000; 2000US-0206129.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Cargill M, Ireland JS, Lander ES;
XX
DR WPI; 2001-522952/57.

```
XX
PT   Nucleic acid molecules from the human genome which include polymorphic
PT   sites, useful in methods for predicting the presence, absence or
PT   severity of a particular phenotype or disorder (e.g. diabetes)
PT   associated with a particular genotype -
XX
PS   Claim 1; Page 59; 145pp; English.
XX
CC   The invention relates to the identification of nucleic acid molecules
CC   (AAI29513-AAI31314) from the human genome which include polymorphic sites
CC   which can predispose individuals to disease. Various genes from a number
CC   of individuals were resequenced and single nucleotide polymorphisms
CC   (SNPs) in these genes discovered. The method is useful for predicting the
CC   presence, absence or severity of a particular phenotype or disorder (e.g.
CC   diabetes) associated with a particular genotype. The nucleic acids
CC   containing the polymorphic sites may be useful in forensics and paternity
CC   testing.
XX
SQ   Sequence 31 BP; 11 A; 6 C; 7 G; 7 T; 0 other;


  Query Match             62.3%;  Score 16.2;  DB 22;  Length 31;
  Best Local Similarity   85.7%;  Pred. No. 3.4e+02;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       5 tgtggccatctttgtccagca 25
           |||| ||||||||| | ||||
Db       9 tgtgaccatctttgacaagca 29


RESULT   2
AAI29682/c
ID   AAI29682 standard; DNA; 31 BP.
XX
AC   AAI29682;
XX
DT   18-OCT-2001  (first entry)
XX
DE   Human single nucleotide polymorphism (SNP) KCNJ2 6.
XX
KW   Human; resequence; genotype; disease; forensic; paternity testing;
KW   single nucleotide polymorphism; SNP; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(16,T)
FT                   /*tag= a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200166800-A2.
XX
PD   13-SEP-2001.
XX
PF   07-MAR-2001; 2001WO-US07268.
XX
PR   07-MAR-2000; 2000US-0187510.
PR   22-MAY-2000; 2000US-0206129.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Cargill M,  Ireland JS,  Lander ES;
XX
DR   WPI; 2001-522952/57.
XX
PT   Nucleic acid molecules from the human genome which include polymorphic
PT   sites, useful in methods for predicting the presence, absence or
PT   severity of a particular phenotype or disorder (e.g. diabetes)
PT   associated with a particular genotype -
XX
PS   Claim 1; Page 40; 145pp; English.
XX
CC   The invention relates to the identification of nucleic acid molecules
CC   (AAI29513-AAI31314) from the human genome which include polymorphic sites
CC   which can predispose individuals to disease. Various genes from a number
CC   of individuals were resequenced and single nucleotide polymorphisms
CC   (SNPs) in these genes discovered. The method is useful for predicting the
CC   presence, absence or severity of a particular phenotype or disorder (e.g.
CC   diabetes) associated with a particular genotype. The nucleic acids
CC   containing the polymorphic sites may be useful in forensics and paternity
CC   testing.
XX
SQ   Sequence 31 BP; 9 A; 6 C; 8 G; 8 T; 0 other;


  Query Match             60.0%;  Score 15.6;  DB 22;  Length 31;
  Best Local Similarity   81.8%;  Pred. No. 6.3e+02;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 ttattgtggccatctttgtcca 22
           |||  |||||||||||| | ||
Db      30 TTACAGTGGCCATCTTTCTTCA 9


RESULT   3
AAF57498
ID   AAF57498 standard; DNA; 51 BP.
XX
AC   AAF57498;
XX
DT   11-JUN-2001  (first entry)
XX
DE   Oprl gene amplifying primer.
XX
KW   Bacteriophage; pseudovirion; phagemid; pathogen; antibacterial;
KW   camel; Oprl; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200121817-A1.
XX
PD   29-MAR-2001.
XX
PF   22-SEP-2000; 2000WO-EP09277.
XX
PR   24-SEP-1999;   99EP-0402348.
PR   03-NOV-1999;   99US-0433404.
XX
PA   (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI   Muyldermans S,  Silence K,  Steyaert J,  Toreele E;
XX
DR   WPI; 2001-257995/26.
XX
PT   New genetically modified bacteriophage, pseudovirion or phagemid
PT   capable of entering host cell by binding of its artificial ligand to
PT   artificial receptor present on host cell, useful for eliminating
PT   specific bacterial population  -
XX
PS   Example 11; Page 35; 69pp; English.
XX
CC   The invention provides a genetically modified bacteriophage, pseudovirion
CC   or phagemid (I) capable of entering a host cell by binding of its
CC   artificial ligand (AL) to an artificial receptor (AR) present on the host
CC   cell. (I) is useful for detecting and/or eliminating a specific bacterial
CC   population, by AR-AL interaction, and to screen an antigen and/or
CC   antibody library. (I) is useful for selecting AR-AL interactions. A kit
CC   comprising (I) is useful for simultaneous in vivo panning of antibody or
CC   antibody fragment library or antigenic sequences library. (I) is useful
CC   for specific elimination of pathogenic bacteria, e.g., Aeromonas,
CC   Enterococcus, Legionella, Listeria, Neisseria, etc and for screening a
CC   host cell, displaying a bait against a library of bacteriophages/
CC   pseudovirions/phagemids displaying the preys. Sequences AAF57497-498
CC   represent PCR primers for amplifying the gene coding for Oprl.
XX
SQ   Sequence 51 BP; 7 A; 16 C; 13 G; 15 T; 0 other;
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  Query Match            57.7%;  Score 15;  DB 22;  Length 51;
  Best Local Similarity  78.3%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       4 ttgtggccatctttgtccagcat 26
           ||| |||   |||| ||||||||
Db      26 ttgcggctggctttttccagcat 48


RESULT   4
AAQ49390
ID   AAQ49390 standard; DNA; 55 BP.
XX
AC   AAQ49390;
XX
DT   06-MAY-1994  (first entry)
XX
DE   PA oligonucleotide CS5M/CS5R.
XX
KW   Tissue plasminogen activator; t-PA; urinary plasminogen activator;
KW   u-PA; fibrin; fibrinogen; thrombolysis; thrombus; resistance;
KW   plasminogen activation factor inhibiting factor 1; ds.
XX
OS   Synthetic.
XX
PN   WO9320194-A.
XX
PD   14-OCT-1993.
XX
PF   03-APR-1992;   92WO-JP00415.
XX
PR   03-APR-1992;   92WO-JP00415.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
XX
PI   Agui H,  Negoro T,  Sato H,  Sudo Y,  Takahashi S;
XX
DR   WPI; 1993-336902/42.
XX
PT   Tissue plasminogen activator analog improved in fibrin
PT   specificity - obtd. by replacing part of aminoacid sequence with
PT   corresponding aminoacid sequence of urinary plasminogen activator
XX
PS   Disclosure; Fig 6; 41pp; Japanese.
XX
CC   The 5' end of the sense strand (CS5M) overhangs the antisense
CC   strand (CS5R) by five bases and the 5' end of the antisense
CC   strand overhangs the sense strand by two bases.
CC   T-PA analogue has at least part of natural t-PA (276-306)
CC   substd. with corresp. amino acid sequence of u-PA (159-188).
CC   The analogue hardly causes activation of plasminogen (and hence
CC   decomposition of fibrinogen), while in circulation (blood).
CC   It activates plasminogen to cause thrombolyis when it reaches the
CC   locus of the thrombus where fibrin is present.  It has high fibrin,
CC   and therefore thrombus specificity and is not expected to cause
CC   general bleeding as side effect.  It also is resistant to plasminogen
CC   activation factor inhibiting factor 1.  Therefore, the analogue will
CC   be a safe thrombolytic agent.
XX
SQ   Sequence 55 BP; 10 A; 14 C; 20 G; 11 T; 0 other;


  Query Match            56.9%;  Score 14.8;  DB 14;  Length 55;
  Best Local Similarity  88.9%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       8 ggccatctttgtccagca 25
           |||||||||||  | ||||
Db       1 ggccatctttgccaagca 18


RESULT   5
AAZ10584/c
ID   AAZ10584 standard; DNA; 36 BP.
XX
AC   AAZ10584;
XX
DT   17-NOV-1999  (first entry)
XX
DE   PCR primer used to create maltogenic alpha amylase mutant F284K.
XX
KW   Maltogenic alpha-amylase; variant; dough additive; bread staling;
KW   starch retrogradation; organoleptic property; detergent; sweetener;
KW   linear oligosaccharide production; ethanol; starch; textile desizing;
KW   PCR primer; ss.
XX
OS   Bacillus sp.
XX
PN   WO9943794-A1.
XX
PD   02-SEP-1999.
XX
PF   26-FEB-1999;   99WO-DK00088.
XX
PR   27-FEB-1998;   98DK-0000269.
PR   12-MAR-1998;   98US-0077795.
XX
PA   (NOVO ) NOVO-NORDISK AS.
XX
PI   Cherry JR,  Svendsen A,  Andersen C,  Beier L,  Frandsen TP;
XX
DR   WPI; 1999-550868/46.
XX
PT   New variants of maltogenic alpha-amylase, particularly used as dough
PT   additives to retard staling  -
XX
PS   Example 1; Page 141; 145pp; English.
XX
CC   The present PCR primer was used to create variants of a maltogenic
CC   alpha-amylase. The specification describes variants of maltogenic
CC   alpha-amylases, which are at least 70% identical to the encoded
CC   protein. The variants have altered pH-dependent activity, improved
CC   stability or higher specific amylase activity than the original amylase.
CC   The variants are used as dough additives to reduce retrogradation
CC   of starch and/or staling of bread. In bread they should result in
CC   increased volume and improved organoleptic properties (flavor,
CC   mouthfeel, palatability, aroma and crust color). Other uses
CC   are in detergents; production of linear oligosaccharides;
CC   production of sweeteners or ethanol from starch; and textile
CC   desizing.
XX
SQ   Sequence 36 BP; 10 A; 6 C; 11 G; 9 T; 0 other;


  Query Match            56.2%;  Score 14.6;  DB 20;  Length 36;
  Best Local Similarity  81.0%;  Pred. No. 1.8e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       5 tgtggccatctttgtccagca 25
           ||| |  |||||| |||||||
Db      31 TGTTGAGATCTTTATCCAGCA 11


RESULT   6
AAF77170/c
ID   AAF77170 standard; DNA; 36 BP.
XX
AC   AAF77170;
XX
DT   23-MAY-2001  (first entry)
XX
DE   Primer F284K.
XX
KW   Maltose; starch; syrup; fat substitute; mutant; mutein; ss.
```

XX
OS Bacillus sp.
XX
PN WO200116349-A1.
XX
PD 08-MAR-2001.
XX
PF 21-AUG-2000; 2000WO-DK00461.
XX
PR 01-SEP-1999; 99DK-0001220.
PR 12-JAN-2000; 2000DK-0000035.
XX
PA (NOVO) NOVOZYMES AS.
XX
PI Pedersen S, Vang Hendriksen H;
XX
DR WPI; 2001-257704/26.
XX
PT Preparation of maltose and modified starch, useful e.g. for paper
PT coating and in food processing, by treating starch with modified
PT Bacillus maltogenic amylase -
XX
PS Example 1; Page 90; 99pp; English.
XX
CC The present invention relates to preparation of maltose and/or
CC modified starch by treating starch with a variant of a maltogenic
CC amylase. The method is used to produce high or low maltose
CC syrups or speciality syrups, useful e.g. in baking and brewing. Also
CC used to make starch for use in coating/sizing paper and in food products
CC (beverages, beverage flavour concentrates and flavouring agents), as a
CC fat substitute and to make maltose for use e.g. in intravenous feeding
CC solutions or as intermediate for the sweetener maltitol.
XX
SQ Sequence 36 BP; 10 A; 6 C; 11 G; 9 T; 0 other;

Query Match 56.2%; Score 14.6; DB 22; Length 36;
Best Local Similarity 81.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 tgtggccatctttgtccagca 25
||| | |||||| |||||||
Db 31 TGTTGAGATCTTTATCCAGCA 11

RESULT 7
AAZ44577
ID AAZ44577 standard; DNA; 20 BP.
XX
AC AAZ44577;
XX
DT 07-APR-2000 (first entry)
XX
DE Newcastle disease virus LaSota primer p1898-.
XX
KW Avian-paramyxovirus; infection; lentogenic; F protein; vaccine;
KW respiratory disease; gastrointestinal disease; poultry pathogen;
KW local immunity; primer; ss.
XX
OS Newcastle disease virus.
XX
PN WO9966045-A1.
XX
PD 23-DEC-1999.
XX
PF 17-JUN-1999; 99WO-NL00377.
XX
PR 19-JUN-1998; 98EP-0202054.
XX
PA (DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOE.
XX
PI Peeters BPH, De Leeuw OS, Koch G, Gielkens ALJ;
XX
DR WPI; 2000-106102/09.
XX
PT New avian paramyxovirus cDNA, useful for production of vaccine against
PT Newcastle disease virus -
XX
PS Disclosure; Page 78; 115pp; English.
XX
CC This invention describes a novel avian-paramyxovirus cDNA (I) which
CC comprises a nucleic acid sequence corresponding to the 5' terminal
CC end of the genome of avian-paramyxovirus allowing the generation of
CC an infectious copy of avian-paramyxovirus. The cell line is useful for
CC the production of infectious lentogenic NDV (Newcastle Disease virus)
CC without the addition of exogenous proteolytic activity. Also it is
CC possible to generate a stable transfected cell line that expresses the
CC wild-type F protein in the virus envelope therefore providing infectious
CC particles, useful in the form of a vaccine, especially against
CC respiratory and/or gastrointestinal diseases. NDV can be easily cultured
CC to very high titers in embryonated eggs. Mass culture of embryonated
CC eggs is relatively cheap. NDV vaccines are relatively stable and can be
CC simply administered by mass application methods e.g. drinking water or
CC by spraying or by aerosol formation. The natural route of infection is
CC by the respiratory and/or gastrointestinal tract which are also the
CC major routes of infection of many other poultry pathogens. NDV can induce
CC local immunity despite the presence of circulating maternal antibody.
CC AAZ44527-Z44609 and AAZ44618-Z44650 represent primers used in the
CC isolation of the NDV strain LaSota genome.
XX
SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 other;

Query Match 55.4%; Score 14.4; DB 21; Length 20;
Best Local Similarity 93.8%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 gtggccatctttgtcc 21
||||||| |||||||
Db 5 gtggccatgtttgtcc 20

RESULT 8
AAT50769/c
ID AAT50769 standard; cDNA; 30 BP.
XX
AC AAT50769;
XX
DT 24-SEP-1997 (first entry)
XX
DE Ovine IL-12 40 kD subunit, reverse primer.
XX
KW Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;
KW livestock; cow; stress; transport; vaccine adjuvant; veterinary;
KW cancer; immunosuppression; allergy; reproductive system; growth;
KW early maturity; antibody; diagnosis; immunopotentiator; PCR; amplify;
KW early haematopoietic progenitor cell; cytotoxic cell; thymocyte;
KW secretion; IgM; IgA; bacterial endotoxin; gamma-interferon; ss.
XX
OS Synthetic.
XX
PN WO9700321-A1.
XX
PD 03-JAN-1997.
XX
PF 14-JUN-1996; 96WO-AU00360.
XX
PR 27-OCT-1995; 95AU-0006244.
PR 14-JUN-1995; 95AU-0003502.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Seow H, Wood P;
XX
DR WPI; 1997-077528/07.
XX

PT Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine
PT adjuvants and to treat or prevent microbial infections in livestock
XX
PS Example 5; Page 27; 78pp; English.
XX
CC The sequences given in AAT50760-69 are primers which were used to
CC amplify the sequences encoding ovine interleukin-5 (IL-5), and
CC interleukin-12 (IL-12) 35 kD subunit (partial and full length sequence)
CC and the 40 kD subunit. Ovine IL-5 or IL-12 are used to treat and/or
CC prevent infections in livestock (esp. cows and sheep), particularly where
CC the animals are stressed, e.g. during transport. IL-5 and IL-12 can also
CC be used as adjuvants in vaccines for veterinary use (partic. weakly
CC immunogenic subunit or synthetic peptide vaccines). They may also be used
CC to treat cancer, immunosuppression and allergy, to enhance/suppress the
CC reproductive system and to promote growth or early maturity. Optionally
CC interleukin can be delivered from constructs or delivery cells and
CC antibodies are useful in enzyme immunoassays for rapid diagnosis of
CC infection. The interleukins are immunopotentiators, especially IL-5
CC promotes growth of early haematopoietic progenitor cells and generation
CC of cytotoxic cells from thymocytes, also it stimulates production and
CC secretion of IgM and IgA (in synergism with bacterial endotoxin).
CC IL-12 induces production of gamma-interferon by, and proliferation
CC of, T and NK cells and increases the (non-)specific cytolytic
CC lymphocyte response. The genetic constructs can also be used for
CC in vitro production of IL-5 or -12.
XX
SQ Sequence 30 BP; 8 A; 11 C; 8 G; 3 T; 0 other;

Query Match 54.6%; Score 14.2; DB 18; Length 30;
Best Local Similarity 84.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 tggccatctttgtccagca 25
||| ||||| ||||| |||
Db 30 TGGGCATCTGTGTCCTGCA 12

RESULT 9
AAV13827/c
ID AAV13827 standard; DNA; 39 BP.
XX
AC AAV13827;
XX
DT 14-MAY-1998 (first entry)
XX
DE Primer for canine IL-12 P40 subunit cDNA.
XX
KW Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW antiviral; vaccine adjuvant; PCR primer; ss.
XX
OS Synthetic.
OS Canis sp.
XX
PN JP10036397-A.
XX
PD 10-FEB-1998.
XX
PF 08-NOV-1996; 96JP-0296789.
XX
PR 23-MAY-1996; 96JP-0128104.
PR 08-NOV-1995; 95JP-0289729.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 1998-174914/16.
XX
PT Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT activities are expected
XX
PS Example 2; Page 6; 12pp; Japanese.
XX
CC The present sequence is a primer for a cDNA encoding a canine
CC interleukin-12 (IL-12) P40 subunit. A canine IL-12 comprising a P40
CC and P35 subunit is capable of inducing an antiviral activating
CC factor and the expression of class II MHC molecules in canine
CC tumour cells, stimulating proliferation of canine blastogenic
CC lymphocytes and activating canine leukocytes to inhibit canine
CC tumour cells. The canine IL-12 can be used in veterinary medicines,
CC e.g. antitumour, antivirus and vaccine adjuvant activities are
CC expected.
XX
SQ Sequence 39 BP; 10 A; 14 C; 8 G; 7 T; 0 other;

Query Match 54.6%; Score 14.2; DB 19; Length 39;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 tggccatctttgtccagca 25
||| ||||| ||||| |||
Db 33 TGGGCATCTGTGTCCTGCA 15

RESULT 10
AAX35628/c
ID AAX35628 standard; cDNA to mRNA; 39 BP.
XX
AC AAX35628;
XX
DT 09-JUL-1999 (first entry)
XX
DE PCR primer for nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW tumour; skin disease; infectious disease; allergic disease;
KW PCR primer; ss.
XX
OS Synthetic.
OS Canis sp.
XX
PN JP11106350-A.
XX
PD 20-APR-1999.
XX
PF 15-MAY-1998; 98JP-0133345.
XX
PR 07-AUG-1997; 97JP-0213755.
PR 16-MAY-1997; 97JP-0127690.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 1999-308068/26.
XX
PT A prevention and treating agent containing interleukin 12 (CaIL12) -
PT for prevention and treatment of dog and cat immune diseases
XX
PS Example 2; Page 7; 16pp; Japanese.
XX
CC PCR primers AAX35627-28 were used to amplify nucleic acid encoding a
CC canine interleukin-12 (IL-12). The specification describes a method
CC for the prevention and treatment of dog and cat immune diseases.
CC The treatment used an agent comprising dog IL-12 (CaIL12) proteins
CC to form a heterodimer. The agent is useful for preventing and treating
CC dog and cat immune diseases, including tumours, skin diseases,
CC infectious diseases and allergic diseases.
XX
SQ Sequence 39 BP; 10 A; 14 C; 8 G; 7 T; 0 other;

Query Match 54.6%; Score 14.2; DB 20; Length 39;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 tggccatctttgtccagca 25

```
          ||| ||||| ||||| |||
Db     33 TGGGCATCTGTGTCCTGCA 15


RESULT  11
AAX03165/c
ID   AAX03165 standard; DNA; 39 BP.
XX
AC   AAX03165;
XX
DT   30-MAR-1999  (first entry)
XX
DE   PCR primer used to amplify a 990 bp fragment of canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; PCR primer; ss.
XX
OS   Synthetic.
OS   Canis sp.
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP02031.
XX
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Example 2; Page 12; 45pp; Japanese.
XX
CC   PCR primers AAX03164-65 were used to amplify a canine interleukin 12
CC   (IL-12) protein cDNA sequence. The IL-12 protein can be used in
CC   therapeutic or prophylactic agents. The agents can be used to prevent
CC   and treat canine and feline immunological diseases including dog and
CC   cat tumours, skin diseases, viral infections and allergic diseases,
CC   especially tumours, breast tumour, oesinophilic granuloma, epidermoid
CC   tumour, skin tumour, lipoma, othematoma, pneumonoedema, skin soft
CC   pedicled soft tumour and anal tumour; skin diseases, otitis externa,
CC   dermatitis, eczema, fungal diseases of the skin, pyoderma, allergic
CC   dermatitis, nettle rash, traumatic dermatitis and hair loss; infections;
CC   dog Parvovirus infection and distemper virus, cat plaque virus infection
CC   and feline leukaemia, and allergic diseases, e.g. pollinosis.
XX
SQ   Sequence 39 BP; 10 A; 14 C; 8 G; 7 T; 0 other;


  Query Match            54.6%;  Score 14.2;  DB 20;  Length 39;
  Best Local Similarity  84.2%;  Pred. No. 2.7e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      7 tggccatctttgtccagca 25
          ||| ||||| ||||| |||
Db     33 TGGGCATCTGTGTCCTGCA 15


RESULT  12
AAV16084
ID   AAV16084 standard; DNA; 43 BP.
XX
AC   AAV16084;
XX
DT   21-MAY-1998  (first entry)
XX
DE   PCR primer used to identify PAX6 mutations in mice.
XX
KW   Mutation; mutational screening; recessive; phenotypic alteration;
KW   single strand conformation polymorphism; SSCP; PAX6 gene; aniridia;
KW   PCR primer; amplify; ss.
XX
OS   Synthetic.
OS   Mus sp.
XX
PN   WO9744485-A1.
XX
PD   27-NOV-1997.
XX
PF   16-MAY-1997;   97WO-GB01354.
XX
PR   17-MAY-1996;   96GB-0010355.
XX
PA   (HEXA-) HEXAGEN TECHNOLOGY LTD.
XX
PI   Goodfellow PN;
XX
DR   WPI; 1998-018536/02.
XX
PT   Identification of mutation(s) in genes of interest - without prior
PT   observation of phenotypic alteration in the mutated organism or cell
XX
PS   Example 11; Page 58; 66pp; English.
XX
CC   PCR primers AAV16059-76 were used to identify PAX6 mutations in mice
CC   using the method of the invention. The method comprises testing a
CC   nucleic acid sample from a mutated organism for a mutation in
CC   a gene of interest without the prior observation of a phenotypic
CC   alteration in the mutated organism resulting from the mutation.
CC   PAX6 mutations lead to a variety of anterior segment malformations most
CC   commonly characterised by eye development defects broadly described as
CC   aniridia. The disease is dominant. A population of male mice were
CC   treated with ENU to provide a source of mutant PAX6 and a heterozygotic
CC   F1 generation produced. Fluorescent single strand conformation
CC   polymorphism (SSCP) is utilised to identify those members of the F1
CC   population carrying PAX6 mutations. The method provides mutational
CC   screening based on genomic and genetic techniques rather than on
CC   phenotypic observation. The method identifies and characterises genes via
CC   mutagenesis to identify genes encoding products which may have
CC   therapeutic benefit. The method also identifies the presence of mutations
CC   in a gene which do not rely solely upon prior matching of a gene with a
CC   disease. Heterozygotic organisms can also be screened to identify those
CC   carrying a mutation in a copy of a gene of interest even though the gene
CC   may be recessive and therefore causes no phenotypic alteration.
XX
SQ   Sequence 43 BP; 12 A; 14 C; 7 G; 10 T; 0 other;


  Query Match            54.6%;  Score 14.2;  DB 19;  Length 43;
  Best Local Similarity  84.2%;  Pred. No. 2.7e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      5 tgtggccatctttgtccag 23
          | || |||||||| |||||
Db     12 tatgaccatctttctccag 30


RESULT  13
AAA05400
ID   AAA05400 standard; DNA; 43 BP.
XX
AC   AAA05400;
XX
```

DT 19-MAY-2000 (first entry)
XX
DE PCR primer Pax6Mm200r used in Pax6 amplimer generation.
XX
KW PCR primer; Sox-2; Sox-3; T gene; Tyrosinase; MGF; Sry; c-kit; Tryp-1;
KW Pax-6; mutation detection; therapeutic target identification; mouse;
KW mast cell growth factor; ss.
XX
OS Mus sp.
XX
PN US6015670-A.
XX
PD 18-JAN-2000.
XX
PF 14-NOV-1997; 97US-0970740.
XX
PR 17-MAY-1996; 96US-0017824.
PR 16-MAY-1997; 97US-0857946.
XX
PA (HEXA-) HEXAGEN TECHNOLOGY LTD.
XX
PI Goodfellow PN;
XX
DR WPI; 2000-181139/16.
XX
PT Detecting mutations in selected genes, useful e.g. for identifying
PT therapeutic targets or products, by analysing DNA in mutated embryonic
PT stem cells without phenotypic characterization -
XX
PS Example 13; Column 51-52; 66pp; English.
XX
CC PCR primers AAA05245-A05406 are used to generate amplimers from the
CC mouse Sox-3 gene, Sox-2 gene, T gene, tyrosinase gene, Tryp-1 gene, Sry
CC gene, MGF (mast cell growth factor) gene, c-kit gene, and the Pax-6 gene.
CC The primers are used in a method for the identification of a mutation in
CC a selected gene in a tissue without the prior observation of a
CC phenotypic alteration in the mutated organism or cell. The method is used
CC to identify mutations in a selected gene that encode products of
CC potential therapeutic activity or that are potential targets,
CC particularly where the gene of interest has been identified as a
CC candidate gene by positional cloning. Other applications are determining
CC functions of genes; detecting the range of phenotypes associated with
CC different mutations in a particular gene and identification of
CC particular mutations. Animals containing an identified mutation are used
CC as models for studying diseases or their treatment, and cells from them
CC for in vitro assessment of drug action. Interbreeding of mutant mice is
CC used to investigate genetic interaction in the overall phenotype.
XX
SQ Sequence 43 BP; 12 A; 14 C; 7 G; 10 T; 0 other;

Query Match 54.6%; Score 14.2; DB 21; Length 43;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 tgtggccatctttgtccag 23
| || |||||||| |||||
Db 12 tatgaccatctttctccag 30

RESULT 14
AAZ43415
ID AAZ43415 standard; DNA; 43 BP.
XX
AC AAZ43415;
XX
DT 11-FEB-2000 (first entry)
XX
DE Murine c-Kit gene PCR primer 32.
XX
KW Screening; mutation; treatment; disease; drug discovery;
KW PCR primer; ss.
XX
OS Mus musculus.
XX
PN US5994075-A.
XX
PD 30-NOV-1999.
XX
PF 16-MAY-1997; 97US-0857946.
XX
PR 17-MAY-1996; 96US-0017824.
XX
PA (HEXA-) HEXAGEN TECHNOLOGY LTD.
XX
PI Goodfellow PN;
XX
DR WPI; 2000-038255/03.
XX
PT Identifying a mutation in a gene of interest in an organism useful for
PT identifying genes encoding products which may have therapeutic benefits
PT -
XX
PS Example 12; Column 127-128; 70pp; English.
XX
CC This invention describes a novel mutational screening method based on
CC genomic and genetic techniques to identify and characterize a mutation
CC in a gene of interest without first selecting a phenotypic
CC characteristic. The screening methods are useful for identifying genes
CC encoding products which may have therapeutic benefit for treating human
CC or animal diseases. The method can be used for the DNA mutation
CC screening of a class or a family of genes providing a rapid assay for
CC identifying mutant genes. The methods produce organisms which can be used
CC for drug discovery e.g. providing a model for the study and treatment of
CC a disease state, allow in vitro assessment of drug activity and
CC interbreeding of mutants which allow investigation of gene interactions
CC in the overall phenotype. A range of phenotypes associated with different
CC mutations, and specified mutations in a gene of interest can be
CC determined. The method can be adapted to screen for a mutation in two or
CC more genes of interest in an organism. The methods allow mutations in a
CC gene of interest to be identified without having to rely on matching a
CC gene with a disease. AAZ43260-Z43421 represent PCR primers used in the
CC method of the invention.
XX
SQ Sequence 43 BP; 12 A; 14 C; 7 G; 10 T; 0 other;

Query Match 54.6%; Score 14.2; DB 21; Length 43;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 tgtggccatctttgtccag 23
| || |||||||| |||||
Db 12 tatgaccatctttctccag 30

RESULT 15
AAH39264/c
ID AAH39264 standard; DNA; 51 BP.
XX
AC AAH39264;
XX
DT 14-AUG-2001 (first entry)
XX
DE Human SNP flanking oligonucleotide SEQ ID 2060.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; ds.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.

XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US28436.
XX
PR 15-OCT-1999; 99US-0160096.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample -
XX
PS Claim 1; Page 60; 83pp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a fragment of human
CC DNA flanking the site of a single nucleotide polymorphism.
XX
SQ Sequence 51 BP; 16 A; 14 C; 8 G; 12 T; 1 other;

Query Match 54.6%; Score 14.2; DB 22; Length 51;
Best Local Similarity 84.2%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       1 ttattgtggccatctttgt 19
           || | |||||||||||  ||
Db      35 TTGTGGTGGCCATCTTAGT 17
```

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